

Paper Copy Sequence Listing 15414A_v4.ST25.txt
SEQUENCE LISTING

<110> Monsanto Technology LLC

Romano, Charles P

Bogdanova, Natalia N

<120> Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression in Plants

<130> 38-21(15414)

<150> 60/407,428

<151> 2002-08-29

<160> 14

<170> PatentIn version 3.1

<210> 1

<211> 3687

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(3687)

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<220>

<221> misc_feature

<222> (1)..(864)

<223> sequence encoding toxin domain I

<220>

<221> misc_feature

<222> (865)..(1488)

<223> sequence encoding toxin domain II

<220>

<221> misc_feature

<222> (1489)..(1929)

<223> sequence encoding toxin domain III

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<221> misc_feature

<222> (1930)..(3687)

<223> sequence encoding protoxin domain

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att cca acg gta tcg aat cct tcc acg caa atg aat cta tca cca gat      96
Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro Asp
20      25      30

gct cgt att gaa gat agc ttg tgt gta gcc gag gtg aac aat att gat      144
Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile Asp
35      40      45

cca ttt gtt agc gca tca aca gtc caa acg ggt ata aac ata gct ggt      192
Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala Gly
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aga ata ttg ggc gta tta ggt gtg ccg ttt gct gga caa cta gct agt      240
Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala Ser
65      70      75      80

ttt tat agt ttt ctt gtt ggg gaa tta tgg cct agt ggc aga gat cca      288
Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp Pro
85      90      95

tgg gaa att ttc ctg gaa cat gta gaa caa ctt ata aga caa caa gta      336
Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100     105     110

aca gaa aat act agg aat acg gct att gct cga tta gaa ggt cta gga      384
Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu Gly
115     120     125

aga ggc tat aga tct tac cag cag gct ctt gaa act tgg tta gat aac      432
Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp Asn
130     135     140

cga aat gat gca aga tca aga agc att att ctt gag cgc tat gtt gct      480
Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala
145     150     155     160

tta gaa ctt gac att act act gct ata ccg ctt ttc aga ata cga aat      528
Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn
165     170     175

gaa gaa gtt cca tta tta atg gta tat gct caa gct gca aat tta cac      576
Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
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cta tta tta ttg aga gac gca tcc ctt ttt ggt agt gaa tgg ggg atg      624
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195     200     205

gca tct tcc gat gtt aac caa tat tac caa gaa caa atc aga tat aca      672
Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr Thr
210     215     220

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Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu Asn
225     230     235     240

aac tta aga ggg aca aat gct gaa agt tgg ttg cgg tat aat caa ttc      768

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Arg	Arg	Asp	Leu	Thr	Leu	Gly	Val	Leu	Asp	Leu	Val	Ala	Leu	Phe	Pro	
			260					265					270			
agc	tat	gat	act	cgc	act	tat	cca	atc	aat	acg	agt	gct	cag	tta	aca	864
Ser	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Asn	Thr	Ser	Ala	Gln	Leu	Thr	
			275				280					285				
aga	gaa	att	tat	aca	gat	cca	att	ggg	aga	aca	aat	gca	cct	tca	gga	912
Arg	Glu	Ile	Tyr	Thr	Asp	Pro	Ile	Gly	Arg	Thr	Asn	Ala	Pro	Ser	Gly	
			290			295					300					
ttt	gca	agt	acg	aat	tgg	ttt	aat	aat	aat	gca	cca	tcg	ttt	tct	gcc	960
Phe	Ala	Ser	Thr	Asn	Trp	Phe	Asn	Asn	Asn	Ala	Pro	Ser	Phe	Ser	Ala	
					310					315					320	
ata	gag	gct	gcc	att	ttc	agg	cct	ccg	cat	cta	ctt	gat	ttt	cca	gaa	1008
Ile	Glu	Ala	Ala	Ile	Phe	Arg	Pro	Pro	His	Leu	Leu	Asp	Phe	Pro	Glu	
				325					330					335		
caa	ctt	aca	att	tac	agt	gca	tca	agc	cgt	tgg	agt	agc	act	caa	cat	1056
Gln	Leu	Thr	Ile	Tyr	Ser	Ala	Ser	Ser	Arg	Trp	Ser	Ser	Thr	Gln	His	
				340				345					350			
atg	aat	tat	tgg	gtg	gga	cat	agg	ctt	aac	ttc	cgc	cca	ata	gga	ggg	1104
Met	Asn	Tyr	Trp	Val	Gly	His	Arg	Leu	Asn	Phe	Arg	Pro	Ile	Gly	Gly	
			355				360					365				
aca	tta	aat	acc	tca	aca	caa	gga	ctt	act	aat	aat	act	tca	att	aat	1152
Thr	Leu	Asn	Thr	Ser	Thr	Gly	Gly	Leu	Thr	Asn	Asn	Thr	Ser	Ile	Asn	
			370				375					380				
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Pro	Val	Thr	Leu	Gln	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg	Thr	Glu	Ser	
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Asn	Ala	Gly	Thr	Asn	Ile	Leu	Phe	Thr	Thr	Pro	Val	Asn	Gly	Val	Pro	
				405					410					415		
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Trp	Ala	Arg	Phe	Asn	Phe	Ile	Asn	Pro	Gln	Asn	Ile	Tyr	Glu	Arg	Gly	
			420					425					430			
gcc	act	acc	tac	agt	caa	ccg	tat	cag	gga	gtt	ggg	att	caa	tta	ttt	1344
Ala	Thr	Thr	Tyr	Ser	Gln	Pro	Tyr	Gln	Gly	Val	Gly	Ile	Gln	Leu	Phe	
			435				440					445				
gat	tca	gaa	act	gaa	tta	cca	cca	gaa	aca	aca	gaa	cga	cca	aat	tat	1392
Asp	Ser	Glu	Thr	Glu	Leu	Pro	Pro	Glu	Thr	Thr	Glu	Arg	Pro	Asn	Tyr	
			450			455					460					
gaa	tca	tat	agt	cat	aga	tta	tct	cat	ata	gga	cta	atc	ata	gga	aac	1440
Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ile	Gly	Asn	
					470				475						480	
act	ttg	aga	gca	cca	gtc	tat	tct	tgg	acg	cat	cgt	agt	gca	gat	cgt	1488
Thr	Leu	Arg	Ala	Pro	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	Asp	Arg	
				485				490					495			
acg	aat	acg	att	gga	cca	aat	aga	att	aca	caa	ata	cca	ttg	gta	aaa	1536
Thr	Asn	Thr	Ile	Gly	Pro	Asn	Arg	Ile	Thr	Gln	Ile	Pro	Leu	Val	Lys	
			500					505					510			
gca	ctg	aat	ctt	cat	tca	ggt	gtt	act	gtt	gtt	gga	ggg	cca	gga	ttt	1584
Ala	Leu	Asn	Leu	His	Ser	Gly	Val	Thr	Val	Val	Gly	Gly	Pro	Gly	Phe	
			515				520					525				
aca	ggt	ggg	gat	atc	ctt	cgt	aga	aca	aat	acg	ggt	aca	ttt	gga	gat	1632
Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	Gly	Asp	
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ata	cga	tta	aat	att	aat	gtg	cca	tta	tcc	caa	aga	tat	cgc	gta	agg	1680
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gga acc act gtt aat att ggt aat ttc tca aga act atg aat agg ggg	1776
Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg Gly	
580 585 590	
gat aat tta gaa tat aga agt ttt aga act gca gga ttt agt act cct	1824
Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr Pro	
595 600 605	
ttt aat ttt tta aat gcc caa agc aca ttc aca ttg ggt gct cag agt	1872
Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln Ser	
610 615 620	
ttt tca aat cag gaa gtt tat ata gat aga gtc gaa ttt gtt cca gca	1920
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625 630 635 640	
gag gta aca ttt gag gca gaa tat gat tta gaa aga gca caa aag gcg	1968
Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala	
645 650 655	
gtg aat gct ctg ttt act tct aca aat cca aga aga ttg aaa aca gat	2016
Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr Asp	
660 665 670	
gtg aca gat tat cat att gac caa gtg tcc aat atg gtg gca tgt tta	2064
Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys Leu	
675 680 685	
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Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys Val	
690 695 700	
aaa tat gcg aag cga ctc agt gat gaa aga aac tta ctc caa gat cca	2160
Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro	
705 710 715 720	
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725 730 735	
caa tca aac ttc ccc tct att aat gag cta tct gaa cat gga tgg tgg	2256
Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp Trp	
740 745 750	
gga agt gcg aat gtt acc att cag gaa ggg aat gac gta ttt aaa gag	2304
Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys Glu	
755 760 765	
aat tac gtc aca cta ccg ggt act ttt aat gag tgt tat cca aat tat	2352
Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn Tyr	
770 775 780	
tta tat caa aaa ata gga gag tca gaa tta aaa gct tat acg cgc tat	2400
Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg Tyr	
785 790 795 800	
caa tta aga ggg tat att gaa gat agt caa gat cta gag att tat tta	2448
Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu	
805 810 815	
att cgt tac aat gca aag cat gaa aca ttg gat gtt cca ggt acc gat	2496
Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr Asp	
820 825 830	
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Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly Glu	
835 840 845	
cca aat cga tgc gca cca cat ttt gaa tgg aat cct gat cta gat tgt	2592
Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp Cys	
850 855 860	
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Ser 865	Cys	Arg	Asp	Gly	Glu 870	Arg	Cys	Ala	His	His 875	Ser	His	His	Phe	Thr 880	
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Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	His	Glu	Asn	Leu	Gly	Val	
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aat	ctg	gaa	ttt	atc	gaa	gag	aaa	cca	tta	att	gga	gaa	gca	ctg	tct	2784
Asn	Leu	Glu	Phe	Ile	Glu	Glu	Lys	Pro	Leu	Ile	Gly	Glu	Ala	Leu	Ser	
		915					920					925				
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Phe	Glu	Glu	Leu	Glu	Gly	His	Ile	Ile	Thr	Ala	Met	Ser	Leu	Tyr		
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Thr	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Gln	Gln	Ser	His		
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His	Arg	Ser	Asp	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser		
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caa	gca	gtt	cggt	gtc	tgt	ccg	ggg	cggt	ggc	tatt	atc	ctt	cggt	gtc		3249
Gln	Ala	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val		
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Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His		
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gaa	atc	gag	aac	aat	aca	gac	gaa	cta	aaa	ttt	aaa	aac	tgt	gaa		3339
Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Lys	Asn	Cys	Glu		
	1100					1105					1110					
gaa	gag	gaa	gtg	tatt	cca	acg	gat	aca	gga	acg	tgt	aat	gat	tatt		3384
Glu	Glu	Glu	Val	Tyr	Pro	Thr	Asp	Thr	Gly	Thr	Cys	Asn	Asp	Tyr		
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act	gca	cac	caagt	aca	gca	gca	tgt	aat	tcc	cggt	aat	gct	gga			3429
Thr	Ala	His	Gln	Gly	Thr	Ala	Ala	Cys	Asn	Ser	Arg	Asn	Ala	Gly		
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tatt	gag	gat	gca	tatt	gaa	ggt	gat	act	aca	gca	tct	ggt	aat	tatt		3474
Tyr	Glu	Asp	Ala	Tyr	Glu	Val	Asp	Thr	Thr	Ala	Ser	Val	Asn	Tyr		
	1145					1150					1155					
aaa	ccg	act	tatt	gaa	gaa	gaa	acg	tatt	aca	gat	gta	cga	aga	gat		3519
Lys	Pro	Thr	Tyr	Glu	Glu	Glu	Thr	Tyr	Thr	Asp	Val	Arg	Arg	Asp		
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Asn His   Cys Glu Tyr Asp Arg   Gly Tyr Val Asn Tyr  Pro Pro Val
  1175                1180                1185

cca gct  ggt tat gtg aca aaa  gaa tta gaa tac ttc  cca gaa aca      3609
Pro Ala   Gly Tyr Val Thr Lys  Glu Leu Glu Tyr Phe  Pro Glu Thr
  1190                1195                1200

gat aca  gta tgg att gag att  gga gaa acg gaa gga  aag ttt att      3654
Asp Thr   Val Trp Ile Glu Ile  Gly Glu Thr Glu Gly  Lys Phe Ile
  1205                1210                1215

gta gat  agc gtg gaa cta ctc  ctc atg gaa gaa                3687
Val Asp   Ser Val Glu Leu Leu  Leu Met Glu Glu
  1220                1225

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<210> 2

<211> 1229

<212> PRT

<213> Bacillus thuringiensis

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<221> misc_feature

<222> (1)..(864)

<223> sequence encoding toxin domain I

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<221> misc_feature

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<223> sequence encoding toxin domain II

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<221> misc_feature

<222> (1489)..(1929)

<223> sequence encoding toxin domain III

<220>

<221> misc_feature

<222> (1930)..(3687)

<223> sequence encoding protoxin domain

<400> 2

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Leu Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser
1          5          10          15

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Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro Asp
          20          25          30

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Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile Asp
35          40          45

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Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala Gly
50          55          60

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Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala Ser
65          70          75          80

Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp Pro
85          90          95

Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val
100         105         110

Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu Gly
115         120         125

Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp Asn
130         135         140

Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala
145         150         155         160

Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn
165         170         175

Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His
180         185         190

Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly Met
195         200         205

Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr Thr
210         215         220

Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu Asn
225         230         235         240

Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe
245         250         255

Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe Pro
260         265         270

Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu Thr
275         280         285

Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly
290         295         300

Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser Ala
305         310         315         320

Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro Glu
325         330         335

Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln His
340         345         350

Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly Gly
355         360         365

Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile Asn
370         375         380

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Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser
385 390 395 400

Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val Pro
405 410 415

Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg Gly
420 425 430

Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu Phe
435 440 445

Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr
450 455 460

Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly Asn
465 470 475 480

Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg
485 490 495

Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val Lys
500 505 510

Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly Phe
515 520 525

Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly Asp
530 535 540

Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val Arg
545 550 555 560

Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile Asn
565 570 575

Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg Gly
580 585 590

Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr Pro
595 600 605

Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln Ser
610 615 620

Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro Ala
625 630 635 640

Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala
645 650 655

Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr Asp
660 665 670

Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys Leu
675 680 685

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Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys Val
690                               695                               700

Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro
705                               710                               715                               720

Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp Gly
725                               730                               735

Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp Trp
740                               745                               750

Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys Glu
755                               760                               765

Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn Tyr
770                               775                               780

Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg Tyr
785                               790                               795                               800

Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu
805                               810                               815

Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr Asp
820                               825                               830

Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly Glu
835                               840                               845

Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp Cys
850                               855                               860

Ser Cys Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe Thr
865                               870                               875                               880

Leu Asp Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly Val
885                               890                               895

Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu Gly
900                               905                               910

Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu Ser
915                               920                               925

Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu
930                               935                               940

Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val Asp
945                               950                               955                               960

Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn
965                               970                               975

Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg Glu
980                               985                               990

Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu Ile
995                               1000                               1005

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Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu Tyr
1010 1015 1020

Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly Leu
1025 1030 1035

Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser His
1040 1045 1050

His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser
1055 1060 1065

Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val
1070 1075 1080

Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
1085 1090 1095

Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys Glu
1100 1105 1110

Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr
1115 1120 1125

Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala Gly
1130 1135 1140

Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr
1145 1150 1155

Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp
1160 1165 1170

Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val
1175 1180 1185

Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr
1190 1195 1200

Asp Thr Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile
1205 1210 1215

Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1220 1225

<210> 3

<211> 3690

<212> DNA

<213> artificial sequence

<220>

<223> fully synthetic coding sequence

<220>

<221> CDS

<222> (1)..(3690)

<223> fully synthetic nucleotide sequence encoding a Cry1Bb amino acid sequence variant

<400> 3

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Met Ala Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu	
1 5 10 15	
tcg atc ccc acg gtc tcg aac ccg tcc acc caa atg aac ctg tcc ccg	96
Ser Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro	
20 25 30	
gac gcc cgc atc gag gac tcc ctg tgc gtc gcg gag gtc aac aac atc	144
Asp Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile	
35 40 45	
gac ccc ttc gtc tcc gcc tcc acg gtc cag acg ggc atc aac atc gct	192
Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala	
50 55 60	
ggc cgc atc ctc ggc gtc ctg ggc gtc ccg ttc gct ggc cag ctg gcc	240
Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala	
65 70 75 80	
tcc ttc tac tcc ttc ctg gtc ggg gag ctg tgg ccc tcc ggt cgc gac	288
Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp	
85 90 95	
ccc tgg gag atc ttc ctg gag cac gtc gag cag ctc atc cgc cag caa	336
Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln	
100 105 110	
gtc acc gag aac acc cgc aac acg gcc atc gcc cgc ctg gag ggc ctg	384
Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu	
115 120 125	
ggc cgt ggc tac cgc tcc tac cag cag gcc ctg gag acc tgg ctg gac	432
Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp	
130 135 140	
aac cgc aac gac gca cgc tcc cgc tcc atc atc ctg gag cgc tac gtg	480
Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val	
145 150 155 160	
gcg ctg gag ctg gac atc acc acc gcc atc ccg ctc ttc cgc atc cgc	528
Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg	
165 170 175	
aat gaa gag gtg ccc ctg ctc atg gtc tac gcc cag gct gcc aac ctg	576
Asn Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu	
180 185 190	
cac ctg ctc ctg ctt cgc gat gca tcc ctg ttc ggc tcc gag tgg ggc	624
His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly	
195 200 205	
atg gcc tcg tcc gac gtc aac cag tac tat cag gag cag atc cgc tac	672
Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr	
210 215 220	
acc gag gag tac tcc aac cac tgc gtc cag tgg tac aac acc ggc ctc	720
Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu	
225 230 235 240	
aac aac ctg cgc ggc acg aac gct gag tcc tgg ctg cgc tac aac cag	768
Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln	
245 250 255	
ttc cgc cgc gac ctg acg ctg ggc gtc ctg gac ctg gtc gcc ctc ttc	816
Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe	
260 265 270	

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ccc tcc tac gac acc cgc acc tac ccc atc aac acg tcc gcc cag ctg	864
Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu	
275 280 285	
acc cgc gag atc tac acc gac ccc atc ggc cgc acc aac gct ccc tcc	912
Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser	
290 295 300	
ggc ttc gcg tcc acg aac tgg ttc aac aac aat gcc ccg tcg ttc tcc	960
Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser	
305 310 315 320	
gcc atc gag gct gcg atc ttc cgc cca ccg cac ctg ctg gac ttc ccc	1008
Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro	
325 330 335	
gag cag ctg acc atc tac tcc gcc tcg tcc cgc tgg tcg tcc acc cag	1056
Glu Gln Leu Thr Ile Tyr Ser Ala Ser Arg Trp Ser Thr Gln	
340 345 350	
cac atg aac tac tgg gtg ggc cac cgc ctg aac ttc agg ccc atc ggt	1104
His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly	
355 360 365	
ggc acc ctg aac acc tcc acc cag ggc ctg acc aac aac acc tcc atc	1152
Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile	
370 375 380	
aac ccc gtc acc ctg cag ttc acg tcc cgc gac gtc tac cgc acc gag	1200
Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu	
385 390 395 400	
tcc aac gcc ggc acc aac atc ctg ttc acg acc ccg gtc aac ggc gtc	1248
Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val	
405 410 415	
ccc tgg gct cgc ttc aac ttc atc aac ccg cag aac atc tac gag cgt	1296
Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg	
420 425 430	
ggt gcg acc acc tac tcc cag ccg tac cag ggc gtc ggc atc cag ctg	1344
Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu	
435 440 445	
ttc gac tcc gag acc gag ctg cca ccc gag acg acc gag cgt ccc aac	1392
Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn	
450 455 460	
tac gag tcc tac tcc cac cgc ctg tcc cac atc ggc ctg atc atc ggc	1440
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly	
465 470 475 480	
aac acc ctg agg gct ccc gtc tac tcc tgg acg cac cgc tcc gcg gac	1488
Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp	
485 490 495	
cgc acg aac acg atc ggt ccc aac cgc atc acc cag atc ccc ctg gtc	1536
Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val	
500 505 510	
aag gcc ctg aac ctg cac tcc ggc gtc acc gtc gtg ggt ggc cca ggc	1584
Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly	
515 520 525	
ttc acc ggt ggc gac atc ctg cgc agg acc aac acg ggc acc ttc ggc	1632
Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly	
530 535 540	
gac atc cgc ctg aac atc aac gtc ccg ctg tcc cag cgc tac cgc gtc	1680
Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val	
545 550 555 560	
cgc atc cgc tac gcc tcc acg acc gac ctg cag ttc ttc acg cgc atc	1728
Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile	
565 570 575	
aac ggc acc acg gtc aac atc ggc aac ttc tcc cgc acc atg aac agg	1776
Asn Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg	

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580	585	590	
ggc gac aac ctg gag tac cgc tcc ttc cgc acc gcc ggc ttc tcc acc Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr 595 600 605			1824
ccg ttc aac ttc ctc aac gcc cag tcc acc ttc acc ctt ggt gcg cag Pro Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln 610 615 620			1872
tcc ttc tcc aac cag gag gtc tac atc gac cgc gtc gag ttc gtc cca Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro 625 630 635 640			1920
gcc gag gtc acc ttc gag gcc gag tac gac ctg gag cgt gcc cag aag Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys 645 650 655			1968
gcg gtg aac gcc ctg ttc acc tcc acc aac ccc agg cgc ctg aag acc Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr 660 665 670			2016
gac gtc acg gac tac cac atc gac cag gtg tcc aac atg gtg gcc tgc Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys 675 680 685			2064
ctc tcc gac gag ttc tgc ctg gac gag aag cgc gag ctg ttc gag aag Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys 690 695 700			2112
gtc aag tac gcg aag cgc ctc tcc gac gag cgc aac ctg ctc cag gac Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp 705 710 715 720			2160
ccg aac ttc acc ttc atc tcc ggc cag ctg tcc ttc gcg tcc atc gac Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp 725 730 735			2208
ggc cag tcc aac ttc ccc tcc atc aac gag ctg tcc gag cac ggc tgg Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp 740 745 750			2256
tgg ggc tcc gcg aac gtc acc atc cag gag ggc aac gac gtc ttc aag Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys 755 760 765			2304
gag aac tac gtc acc ctg ccg ggc acc ttc aac gag tgc tac ccg aac Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn 770 775 780			2352
tac ctc tac cag aag atc ggc gag tcc gag ctg aag gcc tac acc cgc Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg 785 790 795 800			2400
tac cag ctg cgc ggc tac atc gag gac tcc cag gac ctg gag atc tac Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr 805 810 815			2448
ctc atc cgc tac aac gcg aag cac gag acc ctg gac gtc cct ggc acg Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr 820 825 830			2496
gac tcc ctg tgg ccc ctc tcc gtc gag tcg ccc atc ggc cgc tgc ggc Asp Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly 835 840 845			2544
gag ccc aac cgc tgc gct ccc cac ttc gag tgg aac ccc gac ctg gac Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp 850 855 860			2592
tgc tcc tgc cgc gac ggc gag cgc tgc gcg cac cat tcc cat cac ttc Cys Ser Cys Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe 865 870 875 880			2640
acc ctg gac atc gac gtc ggc tgc acc gac ctg cac gag aac ctg ggc Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly 885 890 895			2688

Paper Copy Sequence Listing 15414A_v4.ST25.txt

gtg tgg gtg gtc ttc aag atc aag acg cag gag ggc tac gcc cgc ctg	2736
Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu	
900 905 910	
ggc aac ctg gag ttc atc gag gag aag ccg ctg atc ggc gag gcg ctc	2784
Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu	
915 920 925	
tcc cgc gtc aag cgt gcg gag aag aag tgg cgc gac aag cgc gag aag	2832
Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys	
930 935 940	
ctc cag ctg gag acc aag cgc gtc tac acc gag gcc aag gag gcc gtg	2880
Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val	
945 950 955 960	
gac gcc ctg ttc gtc gac tcc cag tac gac cag ctc cag gcg gac acc	2928
Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr	
965 970 975	
aac atc ggc atg atc cat gcg gct gac aag ctg gtc cac cgc atc cgc	2976
Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg	
980 985 990	
gag gcg tac ctg tcc gag ctg ccc gtc atc cct ggc gtc aac gcg gag	3024
Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu	
995 1000 1005	
atc ttc gag gag ctg gag ggc cac atc atc acc gcc atg tcc ctc	3069
Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu	
1010 1015 1020	
tac gac gcg cgc aac gtg gtc aag aac ggc gac ttc aac aac ggc	3114
Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly	
1025 1030 1035	
ctg acg tgc tgg aac gtc aag ggc cac gtc gac gtc cag caa tcc	3159
Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser	
1040 1045 1050	
cac cac cgc tcc gac ctg gtc atc ccc gag tgg gag gcc gag gtg	3204
His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val	
1055 1060 1065	
tcc cag gcc gtc cgc gtc tgt ccg ggc agg ggc tac atc ctg cgc	3249
Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
1070 1075 1080	
gtc acc gcg tac aag gag ggc tac ggc gag ggc tgc gtc acg atc	3294
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile	
1085 1090 1095	
cac gag atc gag aac aac acc gac gag ctg aag ttc aag aac tgc	3339
His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys	
1100 1105 1110	
gag gag gag gag gtc tac ccg acg gac acc ggc acg tgc aac gac	3384
Glu Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp	
1115 1120 1125	
tac acc gcg cac cag ggc acc gct gcc tgc aac tcc cgc aac gct	3429
Tyr Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala	
1130 1135 1140	
ggc tac gag gac gcc tac gag gtc gac acc acc gcc tcc gtc aac	3474
Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn	
1145 1150 1155	
tac aag ccg acc tac gag gag gag acc tac acc gac gtc cgt cgc	3519
Tyr Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg	
1160 1165 1170	
gac aac cac tgc gag tac gac cgc ggc tac gtg aac tac cca ccc	3564
Asp Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro	
1175 1180 1185	
gtc ccc gct ggc tac gtc acg aag gag ctg gag tac ttc ccc gag	3609
Val Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu	

Paper Copy Sequence Listing 15414A_v4.ST25.txt

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1190          1195          1200
acc gac acc gtc tgg atc gag atc ggc gag acg gag ggc aag ttc 3654
Thr Asp Thr Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe
1205          1210          1215

atc gtc gac tcc gtc gag ctg ctc ctg atg gag gag 3690
Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1220          1225          1230

<210> 4
<211> 1230
<212> PRT
<213> artificial sequence

<220>
<223> fully synthetic coding sequence
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1 5 10 15

Ser Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro
20 25 30

Asp Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile
35 40 45

Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala
50 55 60

Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala
65 70 75 80

Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp
85 90 95

Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln
100 105 110

Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu
115 120 125

Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp
130 135 140

Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val
145 150 155 160

Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg
165 170 175

Asn Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu
180 185 190

His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly
195 200 205

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Paper Copy Sequence Listing 15414A_v4.ST25.txt

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Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr
 210                215                220

Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu
225                230                235                240

Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln
                245                250                255

Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe
                260                265                270

Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu
                275                280                285

Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser
290                295                300

Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser
305                310                315                320

Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro
                325                330                335

Glu Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln
                340                345                350

His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly
355                360                365

Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile
370                375                380

Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu
385                390                395                400

Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val
                405                410                415

Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg
                420                425                430

Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu
435                440                445

Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn
450                455                460

Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly
465                470                475                480

Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp
                485                490                495

Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val
500                505                510

Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly

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515

Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
530 535 540

Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val
545 550 555 560

Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile
565 570 575

Asn Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg
580 585 590

Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr
595 600 605

Pro Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln
610 615 620

Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro
625 630 635 640

Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys
645 650 655

Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr
660 665 670

Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys
675 680 685

Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys
690 695 700

Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
705 710 715 720

Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp
725 730 735

Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp
740 745 750

Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys
755 760 765

Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn
770 775 780

Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg
785 790 795 800

Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr
805 810 815

Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr
820 825 830

Paper Copy Sequence Listing 15414A_v4.ST25.txt

Asp Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly
 835 840 845

 Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp
 850 855 860

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1135

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1370					1375										1380
acg	gac	acc	ggc	acg	tgc	aac	gac	tac	acc	gcg	cac	cag	ggc	acc	6048
Thr	Asp	Thr	Gly	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	His	Gln	Gly	Thr	
1385					1390										1395
gct	gcc	tgc	aac	tcc	cgc	aac	gct	ggc	tac	gag	gac	gcc	tac	gag	6093
Ala	Ala	Cys	Asn	Ser	Arg	Asn	Ala	Gly	Tyr	Glu	Asp	Ala	Tyr	Glu	
1400					1405										1410
gtc	gac	acc	acc	gcc	tcc	gtc	aac	tac	aag	ccg	acc	tac	gag	gag	6138
Val	Asp	Thr	Thr	Ala	Ser	Val	Asn	Tyr	Lys	Pro	Thr	Tyr	Glu	Glu	
1415					1420										1425
gag	acc	tac	acc	gac	gtc	cgt	cgc	gac	aac	cac	tgc	gag	tac	gac	6183
Glu	Thr	Tyr	Thr	Asp	Val	Arg	Arg	Asp	Asn	His	Cys	Glu	Tyr	Asp	
1430					1435										1440
cgc	ggc	tac	gtg	aac	tac	cca	ccc	gtc	ccc	gct	ggc	tac	gtc	acg	6228
Arg	Gly	Tyr	Val	Asn	Tyr	Pro	Pro	Val	Pro	Ala	Gly	Tyr	Val	Thr	
1445					1450										1455
aag	gag	ctg	gag	tac	ttc	ccc	gag	acc	gac	acc	gtc	tgg	atc	gag	6273
Lys	Glu	Leu	Glu	Tyr	Phe	Pro	Glu	Thr	Asp	Thr	Val	Trp	Ile	Glu	
1460					1465										1470
atc	ggc	gag	acg	gag	ggc	aag	ttc	atc	gtc	gac	tcc	gtc	gag	ctg	6318
Ile	Gly	Glu	Thr	Glu	Gly	Lys	Phe	Ile	Val	Asp	Ser	Val	Glu	Leu	
1475					1480										1485
ctc	ctg	atg	gag	gag	tgatagaatt	ctaaatctta	ttattatcat	cgtcgctcgtc							6373
Leu	Leu	Met	Glu	Glu											
1490															
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attcattgat	cactacaaga	gtgatcgact	cgactgtagt	atgtgtgtgc	aatataatgt										6493
gctgtctatc	aacaactact	agtattgtca	tttttttcga	accaggggaac	tttttaatga										6553
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<210> 6

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> fully synthetic expression cassette

<400> 6

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Glu	Arg	Leu	Phe	Gly	Tyr	Asp	Trp	Ala	Gln	Gln	Thr	Ile	Gly	Cys	Ser
		20						25					30		

Asp	Ala	Ala	Val	Phe	Arg	Leu	Ser	Ala	Gln	Gly	Arg	Pro	Val	Leu	Phe
	35						40					45			

Val	Lys	Thr	Asp	Leu	Ser	Gly	Ala	Leu	Asn	Glu	Leu	Gln	Asp	Glu	Ala
	50					55					60				

Ala	Arg	Leu	Ser	Trp	Leu	Ala	Thr	Thr	Gly	Val	Pro	Cys	Ala	Ala	Val
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65              70              75              80
Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
      85              90              95
Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
      100             105             110
Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
      115             120             125
Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
      130             135             140
Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
      145             150             155             160
Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
      165             170             175
Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
      180             185             190
Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
      195             200             205
Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
      210             215             220
Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
      225             230             235             240
Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
      245             250             255
Tyr Arg Leu Leu Asp Glu Phe Phe
      260

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<210> 7

<211> 1230

<212> PRT

<213> Artificial Sequence

<220>

<223> fully synthetic expression cassette

<400> 7

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Ser Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro
      20              25              30
Asp Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile
      35              40              45

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Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala
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 Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala
 65 70 75 80
 Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp
 85 90 95
 Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln
 100 105 110
 Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu
 115 120 125
 Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp
 130 135 140
 Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val
 145 150 155 160
 Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg
 165 170 175
 Asn Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu
 180 185 190
 His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly
 195 200 205
 Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr
 210 215 220
 Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu
 225 230 235 240
 Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln
 245 250 255
 Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe
 260 265 270
 Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu
 275 280 285
 Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser
 290 295 300
 Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser
 305 310 315 320
 Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro
 325 330 335
 Glu Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln
 340 345 350
 His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly

355

Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile
370 375 380

Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu
385 390 395 400

Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val
405 410 415

Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg
420 425 430

Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu
435 440 445

Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn
450 455 460

Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly
465 470 475 480

Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp
485 490 495

Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val
500 505 510

Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly
515 520 525

Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
530 535 540

Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val
545 550 555 560

Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile
565 570 575

Asn Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg
580 585 590

Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr
595 600 605

Pro Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln
610 615 620

Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro
625 630 635 640

Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys
645 650 655

Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr
660 665 670

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Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys
 675 680 685
 Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys
 690 695 700
 Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
 705 710 715 720
 Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp
 725 730 735
 Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp
 740 745 750
 Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys
 755 760 765
 Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn
 770 775 780
 Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg
 785 790 795 800
 Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr
 805 810 815
 Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr
 820 825 830
 Asp Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly
 835 840 845
 Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp
 850 855 860
 Cys Ser Cys Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe
 865 870 875 880
 Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly
 885 890 895
 Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu
 900 905 910
 Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu
 915 920 925
 Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys
 930 935 940
 Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val
 945 950 955 960
 Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr
 965 970 975
 Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg

980

Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu
995 1000 1005

Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu
1010 1015 1020

Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly
1025 1030 1035

Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser
1040 1045 1050

His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val
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Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1070 1075 1080

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
1085 1090 1095

His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys
1100 1105 1110

Glu Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp
1115 1120 1125

Tyr Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala
1130 1135 1140

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn
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Tyr Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg
1160 1165 1170

Asp Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro
1175 1180 1185

Val Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu
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Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
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<210> 8

<211> 7000

<212> DNA

<213> Artificial Sequence

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<223> fully synthetic expression cassette
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<222> (174)..(490)
<223> P-CAMV 35S

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<221> CDS
<222> (526)..(1320)
<223> nptII

<220>
<221> transcription termination & polyadenylation sequence
<222> (1325)..(1767)
<223> T-AGRtu.nos3'

<220>
<221> promoter
<222> (1809)..(2386)
<223> P-FMV

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<221> 5'UTL
<222> (2407)..(2480)
<223> L-Os.betaTUB

<220>
<221> Intron
<222> (2498)..(2614)
<223> I-Os.PAL

<220>
<221> transit_peptide
<222> (2644)..(2790)
<223> TP-Zm.rbcS

<220>
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<222> (2791)..(2953)

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<223> I-Zm.rbcS

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<221> transit_peptide

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<223> TP-Zm.rbcS

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<221> CDS

<222> (3041)..(6730)

<223> Cry1Bb variant

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<221> transcription termination sequence

<222> (6731)..(6736)

<223> miscellaneous sequence

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<221> polyadenylation sequence

<222> (6742)..(6981)

<223> T-Os.LDH

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gtaaaacgac ggccagtga ttcgcggccac gcgtgggtacc aagcttcccg atcctatctg      180
tcacttcattc aaaaggacag tagaaaagga aggtggcacc taaaaatgcc atcattgcga      240
taaaggaaag gctatcattc aagatgcctc tgccgacagt ggtcccaaag atggaccccc      300
acccacgagg agcatcgttg aaaaagaaga cgttccaacc acgtcttcaa agcaagtgga      360
ttgatgtgat acttccactg acgtaaggga atgacgcaca atcccactat ccttcgcaag      420
acccttcctc tatataagga agttcatttc atttgagagag gacacgctga aatcaccagt      480
ctctctctac aagatcgggg atctctagct agacgatcgt ttcgc atg att gaa caa      537
                               Met Ile Glu Gln
                               1

gat gga ttg cac gca ggt tct ccg gcc gct tgg gtg gag agg cta ttc      585
Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe
5                               10                               15                               20

ggc tat gac tgg gca caa cag aca atc ggc tgc tct gat gcc gcc gtg      633
Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val
25                               30                               35

ttc cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt gtc aag acc gac      681
Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp
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Paper Copy Sequence Listing 15414A_v4.ST25.txt

ctg tcc ggt gcc ctg aat gaa ctg cag gac gag gca gcg cgg cta tcg	729
Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser	
55 60 65	
tggtg ctg gcc acg acg ggc gtt cct tgc gca gct gtg ctc gac gtt gtc	777
Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val	
70 75 80	
act gaa gcg gga agg gac tgg ctg cta ttg ggc gaa gtg ccg ggg cag	825
Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln	
85 90 95 100	
gat ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg	873
Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met	
105 110 115	
gct gat gca atg cgg cgg ctg cat acg ctt gat ccg gct acc tgc cca	921
Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro	
120 125 130	
ttc gac cac caa gcg aaa cat cgc atc gag cga gca cgt act cgg atg	969
Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met	
135 140 145	
gaa gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg	1017
Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly	
150 155 160	
ctc gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg cgc atg ccc gac	1065
Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp	
165 170 175 180	
ggc gag gat ctc gtc gtg acc cat ggc gat gcc tgc ttg ccg aat atc	1113
Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile	
185 190 195	
atg gtg gaa aat ggc cgc ttt tct gga ttc atc gac tgt ggc cgg ctg	1161
Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu	
200 205 210	
gggtgtg gcg gac cgc tat cag gac ata gcg ttg gct acc cgt gat att	1209
Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile	
215 220 225	
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Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr	
230 235 240	
gggtatc gcc gct ccc gat tgc cag cgc atc gcc ttc tat cgc ctt ctt	1305
Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg Leu Leu	
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Asp Glu Phe Phe	
caacctgccca tcacgagatt tcgattccac cgccgccttc tatgaaaggt tgggcttcgg	1420
aatcggttttc cgggacgcgg gctggatgat cctccagcgc ggggatctca tgctggagtt	1480
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cggccgcggtt aacaagcttg agctcaggat ttagcagcat tccagattgg gttcaatcaa	1840
caaggtagca gccatatcac tttattcaaa ttggtatcgc caaaaccaag aaggaactcc	1900
catcctcaaa gggtttgtaag gaagaattct cagtccaaag cctcaacaag gtcagggtag	1960
agagtctcca aaccattagc caaaagctac aggagatcaa tgaagaatct tcaatcaaag	2020

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taaactactg ttccagcaca tgcatcatgg tcagtaagtt tcagaaaaag acatccaccg	2080
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acaaaagaat tccctctata taagaaggca ttcattccca tttgaaggat catcagatac	2380
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caatgccggt ctagaggatc agcatggcgc ccaccgtgat gatggcctcg tcggccaccg	2680
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gggaactgat gatccatgca tggactgatg tgtgttgccc atcccatccc atcccatttc	2920
ccaaacgaac cgaaaacacc gtactacgtg caggtgtggc cctacggcaa caagaagttc	2980
gagacgctgt cgtacctgcc gccgctgtcg accggcgggc gcatccgctg catgcaggcc	3040
atg gcc acc tcc aac cgc aag aac gag aat gag atc atc aac gcc ctg	3088
Met Ala Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu	
265 270 275 280	
tcg atc ccc acg gtc tcg aac ccg tcc acc caa atg aac ctg tcc ccg	3136
Ser Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro	
285 290 295	
gac gcc cgc atc gag gac tcc ctg tgc gtc gcg gag gtc aac aac atc	3184
Asp Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile	
300 305 310	
gac ccc ttc gtc tcc gcc tcc acg gtc cag acg ggc atc aac atc gct	3232
Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala	
315 320 325	
ggc cgc atc ctc gcc gtc ctg gcc gtc ccg ttc gct ggc cag ctg gcc	3280
Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala	
330 335 340	
tcc ttc tac tcc ttc ctg gtc ggg gag ctg tgg ccc tcc ggt cgc gac	3328
Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp	
345 350 355 360	
ccc tgg gag atc ttc ctg gag cac gtc gag cag ctc atc cgc cag caa	3376
Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln	
365 370 375	
gtc acc gag aac acc cgc aac acg gcc atc gcc cgc ctg gag ggc ctg	3424
Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu	
380 385 390	
ggc cgt ggc tac cgc tcc tac cag cag gcc ctg gag acc tgg ctg gac	3472
Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp	
395 400 405	
aac cgc aac gac gca cgc tcc cgc tcc atc atc ctg gag cgc tac gtg	3520
Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val	
410 415 420	
gcg ctg gag ctg gac atc acc acc gcc atc ccg ctc ttc cgc atc cgc	3568
Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg	
425 430 435 440	

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445 450 455	
cac ctg ctc ctg ctt cgc gat gca tcc ctg ttc ggc tcc gag tgg ggc	3664
His Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly	
460 465 470	
atg gcc tcg tcc gac gtc aac cag tac tat cag gag cag atc cgc tac	3712
Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr	
475 480 485	
acc gag gag tac tcc aac cac tgc gtc cag tgg tac aac acc ggc ctc	3760
Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu	
490 495 500	
aac aac ctg cgc ggc acg aac gct gag tcc tgg ctg cgc tac aac cag	3808
Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln	
505 510 515 520	
ttc cgc cgc gac ctg acg ctg ggc gtc ctg gac ctg gtc gcc ctc ttc	3856
Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe	
525 530 535	
ccc tcc tac gac acc cgc acc tac ccc atc aac acg tcc gcc cag ctg	3904
Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu	
540 545 550	
acc cgc gag atc tac acc gac ccc atc ggc cgc acc aac gct ccc tcc	3952
Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser	
555 560 565	
ggc ttc gcg tcc acg aac tgg ttc aac aac aat gcc ccg tcg ttc tcc	4000
Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser	
570 575 580	
gcc atc gag gct gcg atc ttc cgc cca ccg cac ctc ctg gac ttc ccc	4048
Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro	
585 590 595 600	
gag cag ctg acc atc tac tcc gcc tcg tcc cgc tgg tcg tcc acc cag	4096
Glu Gln Leu Thr Ile Tyr Ser Ala Ser Arg Trp Ser Ser Thr Gln	
605 610 615	
cac atg aac tac tgg gtg ggc cac cgc ctc aac ttc agg ccc atc ggt	4144
His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly	
620 625 630	
ggc acc ctg aac acc tcc acc cag ggc ctg acc aac aac acc tcc atc	4192
Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile	
635 640 645	
aac ccc gtc acc ctc cag ttc acg tcc cgc gac gtc tac cgc acc gag	4240
Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu	
650 655 660	
tcc aac gcc ggc acc aac atc ctc ttc acg acc ccg gtc aac ggc gtc	4288
Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val	
665 670 675 680	
ccc tgg gct cgc ttc aac ttc atc aac ccg cag aac atc tac gag cgt	4336
Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg	
685 690 695	
ggt gcg acc acc tac tcc cag ccg tac cag ggc gtc ggc atc cag ctc	4384
Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu	
700 705 710	
ttc gac tcc gag acc gag ctg cca ccc gag acg acc gag cgt ccc aac	4432
Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn	
715 720 725	
tac gag tcc tac tcc cac cgc ctg tcc cac atc ggc ctg atc atc ggc	4480
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly	
730 735 740	
aac acc ctc agg gct ccc gtc tac tcc tgg acg cac cgc tcc gcg gac	4528
Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp	

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745	750	755	760	
cgc acg aac acg atc ggt ccc aac cgc atc acc cag atc ccc ctg gtc Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val	765	770	775	4576
aag gcc ctc aac ctg cac tcc ggc gtc acc gtc gtg ggt ggc cca ggc Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly	780	785	790	4624
ttc acc ggt ggc gac atc ctg cgc agg acc aac acg ggc acc ttc ggc Phe Thr Gly Gly Asp Ile Leu Arg Thr Asn Thr Gly Thr Phe Gly	795	800	805	4672
gac atc cgc ctc aac atc aac gtc ccg ctg tcc cag cgc tac cgc gtc Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val	810	815	820	4720
cgc atc cgc tac gcc tcc acg acc gac ctc cag ttc ttc acg cgc atc Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile	825	830	835	4768
aac ggc acc acg gtc aac atc ggc aac ttc tcc cgc acc atg aac agg Asn Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg	845	850	855	4816
ggc gac aac ctg gag tac cgc tcc ttc cgc acc gcc ggc ttc tcc acc Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr	860	865	870	4864
ccg ttc aac ttc ctc aac gcc cag tcc acc ttc acc ctt ggt gcg cag Pro Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln	875	880	885	4912
tcc ttc tcc aac cag gag gtc tac atc gac cgc gtc gag ttc gtc cca Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro	890	895	900	4960
gcc gag gtc acc ttc gag gcc gag tac gac ctg gag cgt gcc cag aag Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys	905	910	915	5008
gcg gtg aac gcc ctg ttc acc tcc acc aac ccc agg cgc ctg aag acc Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr	925	930	935	5056
gac gtc acg gac tac cac atc gac cag gtg tcc aac atg gtg gcc tgc Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys	940	945	950	5104
ctc tcc gac gag ttc tgc ctg gac gag aag cgc gag ctg ttc gag aag Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys	955	960	965	5152
gtc aag tac gcg aag cgc ctc tcc gac gag cgc aac ctg ctc cag gac Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp	970	975	980	5200
ccg aac ttc acc ttc atc tcc ggc cag ctg tcc ttc gcg tcc atc gac Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp	985	990	995	5248
ggc cag tcc aac ttc ccc tcc atc aac gag ctg tcc gag cac ggc Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly	1005	1010	1015	5293
tgg tgg ggc tcc gcg aac gtc acc atc cag gag ggc aac gac gtc Trp Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val	1020	1025	1030	5338
ttc aag gag aac tac gtc acc ctg ccg ggc acc ttc aac gag tgc Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys	1035	1040	1045	5383
tac ccg aac tac ctc tac cag aag atc ggc gag tcc gag ctg aag Tyr Pro Asn Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys	1050	1055	1060	5428

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gcc tac acc cgc tac cag ctg cgc ggc tac atc gag gac tcc cag	5473
Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln	
1065 1070 1075	
gac ctg gag atc tac ctc atc cgc tac aac gcg aag cac gag acc	5518
Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr	
1080 1085 1090	
ctg gac gtc cct ggc acg gac tcc ctg tgg ccc ctc tcc gtc gag	5563
Leu Asp Val Pro Gly Thr Asp Ser Leu Trp Pro Leu Ser Val Glu	
1095 1100 1105	
tcg ccc atc ggc cgc tgc ggc gag ccc aac cgc tgc gct ccc cac	5608
Ser Pro Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His	
1110 1115 1120	
ttc gag tgg aac ccc gag ctg gac tgc tcc tgc cgc gac ggc gag	5653
Phe Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu	
1125 1130 1135	
cgc tgc gcg cac cat tcc cat cac ttc acc ctg gac atc gac gtc	5698
Arg Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp Val	
1140 1145 1150	
ggc tgc acc gac ctg cac gag aac ctg ggc gtg tgg gtg gtc ttc	5743
Gly Cys Thr Asp Leu His Glu Asn Leu Gly Val Trp Val Val Phe	
1155 1160 1165	
aag atc aag acg cag gag ggc tac gcc cgc ctg ggc aac ctg gag	5788
Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu Gly Asn Leu Glu	
1170 1175 1180	
ttc atc gag gag aag ccg ctg atc ggc gag gcg ctc tcc cgc gtc	5833
Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu Ser Arg Val	
1185 1190 1195	
aag cgt gcg gag aag aag tgg cgc gac aag gcg gag aag ctc cag	5878
Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln	
1200 1205 1210	
ctg gag acc aag cgc gtc tac acc gag gcc aag gag gcc gtg gac	5923
Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val Asp	
1215 1220 1225	
gcc ctg ttc gtc gac tcc cag tac gac cag ctc cag gcg gac acc	5968
Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr	
1230 1235 1240	
aac atc ggc atg atc cat gcg gct gac aag ctg gtc cac cgc atc	6013
Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile	
1245 1250 1255	
cgc gag gcg tac ctg tcc gag ctg ccc gtc atc cct ggc gtc aac	6058
Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn	
1260 1265 1270	
gcg gag atc ttc gag gag ctg gag ggc cac atc atc acc gcc atg	6103
Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met	
1275 1280 1285	
tcc ctc tac gac gcg cgc aac gtg gtc aag aac ggc gac ttc aac	6148
Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn	
1290 1295 1300	
aac ggc ctg acg tgc tgg aac gtc aag ggc cac gtc gac gtc cag	6193
Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln	
1305 1310 1315	
caa tcc cac cac cgc tcc gac ctg gtc atc ccc gag tgg gag gcc	6238
Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala	
1320 1325 1330	
gag gtg tcc cag gcc gtc cgc gtc tgt ccg ggc agg ggc tac atc	6283
Glu Val Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile	
1335 1340 1345	
ctg cgc gtc acc gcg tac aag gag ggc tac ggc gag ggc tgc gtc	6328
Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val	

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1350	1355	1360	
acg atc cac gag atc Thr Ile His Glu Ile 1365	gag aac aac acc gag Glu Asn Asn Thr Asp 1370	gag ctg aag ttc aag Glu Leu Lys Phe Lys 1375	6373
aac tgc gag gag gag Asn Cys Glu Glu Glu 1380	gag gtc tac ccg acg Glu Val Tyr Pro Thr 1385	gac acc ggc acg tgc Asp Thr Gly Thr Cys 1390	6418
aac gac tac acc gcg Asn Asp Tyr Thr Ala 1395	cac cag ggc acc gct His Gln Gly Thr Ala 1400	gcc tgc aac tcc cgc Ala Cys Asn Ser Arg 1405	6463
aac gct ggc tac gag Asn Ala Gly Tyr Glu 1410	gac gcc tac gag gtc Asp Ala Tyr Glu Val 1415	gac acc acc gcc tcc Asp Thr Thr Ala Ser 1420	6508
gtc aac tac aag ccg Val Asn Tyr Lys Pro 1425	acc tac gag gag gag Thr Tyr Glu Glu Glu 1430	acc tac acc gac gtc Thr Tyr Thr Asp Val 1435	6553
cgt cgc gac aac cac Arg Arg Asp Asn His 1440	tgc gag tac gac cgc Cys Glu Tyr Asp Arg 1445	ggc tac gtg aac tac Gly Tyr Val Asn Tyr 1450	6598
cca ccc gtc ccc gct Pro Pro Val Pro Ala 1455	ggc tac gtc acg aag Gly Tyr Val Thr Lys 1460	gag ctg gag tac ttc Glu Leu Glu Tyr Phe 1465	6643
ccc gag acc gac acc Pro Glu Thr Asp Thr 1470	gtc tgg atc gag atc Val Trp Ile Glu Ile 1475	ggc gag acg gag ggc Gly Glu Thr Glu Gly 1480	6688
aag ttc atc gtc gac Lys Phe Ile Val Asp 1485	tcc gtc gag ctg ctc Ser Val Glu Leu Leu 1490	ctg atg gag gag Leu Met Glu Glu	6730
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aaagtaccta ctccgtactt agctagctac	aataataagg attcattgat cactacaaga		6850
gtgatcgact cgactgtagt atgtgtgtgc	aatataatgt gctgtctatc aacaactact		6910
agtattgtca tttttttcga accaggggaac	tttttaatga taagaagaaa aagacaagta		6970
cttattgtcg agcatgctg tgtgtttttt			7000

<210> 9

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> fully synthetic expression cassette

<400> 9

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Glu	Arg	Leu	Phe	Gly	Tyr	Asp	Trp	Ala	Gln	Gln	Thr	Ile	Gly	Cys	Ser
		20						25					30		

Asp	Ala	Ala	Val	Phe	Arg	Leu	Ser	Ala	Gln	Gly	Arg	Pro	Val	Leu	Phe
		35					40				45				

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala

50

55

60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

<210> 10

<211> 1230

<212> PRT

<213> Artificial Sequence

<220>

<223> fully synthetic expression cassette

<400> 10

Met Ala Thr Ser Asn Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu
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Ser Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro
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Asp Ala Arg Ile Glu Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile
 35 40 45
 Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala
 50 55 60
 Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala
 65 70 75 80
 Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp
 85 90 95
 Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln
 100 105 110
 Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu
 115 120 125
 Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp
 130 135 140
 Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val
 145 150 155 160
 Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg
 165 170 175
 Asn Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu
 180 185 190
 His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly
 195 200 205
 Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr
 210 215 220
 Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu
 225 230 235 240
 Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln
 245 250 255
 Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe
 260 265 270
 Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu
 275 280 285
 Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser
 290 295 300
 Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser
 305 310 315 320
 Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro
 325 330 335
 Glu Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln

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340

345

350

His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly
355 360 365

Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile
370 375 380

Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu
385 390 395 400

Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val
405 410 415

Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg
420 425 430

Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu
435 440 445

Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn
450 455 460

Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly
465 470 475 480

Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp
485 490 495

Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val
500 505 510

Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly
515 520 525

Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
530 535 540

Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val
545 550 555 560

Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile
565 570 575

Asn Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg
580 585 590

Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr
595 600 605

Pro Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln
610 615 620

Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro
625 630 635 640

Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys
645 650 655

Paper Copy Sequence Listing 15414A_v4.ST25.txt

Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr
660 665 670

Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys
675 680 685

Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys
690 695 700

Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
705 710 715 720

Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp
725 730 735

Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp
740 745 750

Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys
755 760 765

Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn
770 775 780

Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg
785 790 795 800

Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr
805 810 815

Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr
820 825 830

Asp Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly
835 840 845

Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp
850 855 860

Cys Ser Cys Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe
865 870 875 880

Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly
885 890 895

Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu
900 905 910

Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu
915 920 925

Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys
930 935 940

Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val
945 950 955 960

Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr

965

970

975

Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg
 980 985 990

 Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu
 995 1000 1005

 Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu
 1010 1015 1020

 Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly
 1025 1030 1035

 Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser
 1040 1045 1050

 His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val
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 Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1070 1075 1080

 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
 1085 1090 1095

 His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys
 1100 1105 1110

 Glu Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp
 1115 1120 1125

 Tyr Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala
 1130 1135 1140

 Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn
 1145 1150 1155

 Tyr Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg
 1160 1165 1170

 Asp Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro
 1175 1180 1185

 Val Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu
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 1220 1225 1230

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<211> 5170

<212> DNA

<213> Artificial Sequence

<220>

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<221> promoter

<222> (26)..(640)

<223> P-e35S

<220>

<221> 5'UTL

<222> (665)..(735)

<223> L-Ta.CAB

<220>

<221> Intron

<222> (749)..(1239)

<223> I-Os.ACT1

<220>

<221> CDS

<222> (1241)..(4930)

<223> Cry1Bb variant

<220>

<221> transcription_termination_sequence

<222> (4931)..(4936)

<223> miscellaneous

<220>

<221> polyadenylation sequence

<222> (4937)..(5170)

<223> T-Ta.hsp70

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atgcctctgc cgacagtggg cccaaagatg gacccccacc cagaggagc atcgtggaaa	240
aagaagacgt tccaaccacg tcttcaaagc aagtggattg atgtgatggt ccgatgtgag	300

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Met Ala Thr Ser Asn
1 5

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Arg Lys Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser Ile Pro Thr Val
10 15 20

tcg aac ccg tcc acc caa atg aac ctg tcc ccg gac gcc cgc atc gag 1351
Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro Asp Ala Arg Ile Glu
25 30 35

gac tcc ctg tgc gtc gcg gag gtc aac aac atc gac ccc ttc gtc tcc 1399
Asp Ser Leu Cys Val Ala Glu Val Asn Asn Ile Asp Pro Phe Val Ser
40 45 50

gcc tcc acg gtc cag acg ggc atc aac atc gct ggc cgc atc ctc ggc 1447
Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala Gly Arg Ile Leu Gly
55 60 65

gtc ctg ggc gtc ccg ttc gct ggc cag ctg gcc tcc ttc tac tcc ttc 1495
Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe
70 75 80 85

ctg gtc ggg gag ctg tgg ccc tcc ggt cgc gac ccc tgg gag atc ttc 1543
Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp Pro Trp Glu Ile Phe
90 95 100

ctg gag cac gtc gag cag ctc atc cgc cag caa gtc acc gag aac acc 1591
Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln Val Thr Glu Asn Thr
105 110 115

cgc aac acg gcc atc gcc cgc ctg gag ggc ctg ggc cgt ggc tac cgc 1639
Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu Gly Arg Gly Tyr Arg
120 125 130

tcc tac cag cag gcc ctg gag acc tgg ctg gac aac cgc aac gac gca 1687
Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp Asn Arg Asn Asp Ala
135 140 145

cgc tcc cgc tcc atc atc ctg gag cgc tac gtg gcg ctg gag ctg gac 1735
Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu Glu Leu Asp
150 155 160 165

atc acc acc gcc atc ccg ctc ttc cgc atc cgc aat gaa gag gtg ccc 1783
Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu Glu Val Pro
170 175 180

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ctg ctc atg gtc tac gcc cag gct gcc aac ctg cac ctg ctc ctg ctt	1831
Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu Leu Leu	
185 190 195	
cgc gat gca tcc ctg ttc ggc tcc gag tgg ggc atg gcc tcg tcc gac	1879
Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly Met Ala Ser Ser Asp	
200 205 210	
gtc aac cag tac tat cag gag cag atc cgc tac acc gag gag tac tcc	1927
Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr Thr Glu Glu Tyr Ser	
215 220 225	
aac cac tgc gtc cag tgg tac aac acc ggc ctc aac aac ctg cgc ggc	1975
Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu Asn Asn Leu Arg Gly	
230 235 245	
acg aac gct gag tcc tgg ctg cgc tac aac cag ttc cgc cgc gac ctg	2023
Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe Arg Arg Asp Leu	
250 255 260	
acg ctg ggc gtc ctg gac ctg gtc gcc ctc ttc ccc tcc tac gac acc	2071
Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr	
265 270 275	
cgc acc tac ccc atc aac acg tcc gcc cag ctg acc cgc gag atc tac	2119
Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu Thr Arg Glu Ile Tyr	
280 285 290	
acc gac ccc atc ggc cgc acc aac gct ccc tcc ggc ttc gcg tcc acg	2167
Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly Phe Ala Ser Thr	
295 300 305	
aac tgg ttc aac aac aat gcc ccg tcg ttc tcc gcc atc gag gct gcg	2215
Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala	
310 315 325	
atc ttc cgc cca ccg cac ctc ctg gac ttc ccc gag cag ctg acc atc	2263
Ile Phe Arg Pro His Leu Leu Asp Phe Pro Glu Gln Leu Thr Ile	
330 335 340	
tac tcc gcc tcg tcc cgc tgg tcg tcc acc cag cac atg aac tac tgg	2311
Tyr Ser Ala Ser Arg Trp Ser Thr Gln His Met Asn Tyr Trp	
345 350 355	
gtg ggc cac cgc ctc aac ttc agg ccc atc ggt ggc acc ctg aac acc	2359
Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly Gly Thr Leu Asn Thr	
360 365 370	
tcc acc cag ggc ctg acc aac aac acc tcc atc aac ccc gtc acc ctc	2407
Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile Asn Pro Val Thr Leu	
375 380 385	
cag ttc acg tcc cgc gac gtc tac cgc acc gag tcc aac gcc ggc acc	2455
Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu Ser Asn Ala Gly Thr	
390 395 400 405	
aac atc ctc ttc acg acc ccg gtc aac ggc gtc ccc tgg gct cgc ttc	2503
Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val Pro Trp Ala Arg Phe	
410 415 420	
aac ttc atc aac ccg cag aac atc tac gag cgt ggt gcg acc acc tac	2551
Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg Gly Ala Thr Thr Tyr	
425 430 435	
tcc cag ccg tac cag ggc gtc ggc atc cag ctc ttc gac tcc gag acc	2599
Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu Phe Asp Ser Glu Thr	
440 445 450	
gag ctg cca ccc gag acg acc gag cgt ccc aac tac gag tcc tac tcc	2647
Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn Tyr Glu Ser Tyr Ser	
455 460 465	
cac cgc ctg tcc cac atc ggc ctg atc atc ggc aac acc ctc agg gct	2695
His Arg Leu Ser His Ile Gly Leu Ile Ile Gly Asn Thr Leu Arg Ala	
470 475 480 485	
ccc gtc tac tcc tgg acg cac cgc tcc gcg gac cgc acg aac acg atc	2743
Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn Thr Ile	

490	495	500	
ggt ccc aac cgc atc acc cag atc ccc ctg gtc aag gcc ctc aac ctg Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val Lys Ala Leu Asn Leu 505	510	515	2791
cac tcc ggc gtc acc gtc gtg ggt ggc cca ggc ttc acc ggt ggc gac His Ser Gly Val Thr Val Val Gly Gly Pro Gly Phe Thr Gly Gly Asp 520	525	530	2839
atc ctg cgc agg acc aac acg ggc acc ttc ggc gac atc cgc ctc aac Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly Asp Ile Arg Leu Asn 535	540	545	2887
atc aac gtc ccg ctg tcc cag cgc tac cgc gtc cgc atc cgc tac gcc Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala 550	555	560	2935
tcc acg acc gac ctc cag ttc ttc acg cgc atc aac ggc acc acg gtc Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile Asn Gly Thr Thr Val 570	575	580	2983
aac atc ggc aac ttc tcc cgc acc atg aac agg ggc gac aac ctg gag Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg Gly Asp Asn Leu Glu 585	590	595	3031
tac cgc tcc ttc cgc acc gcc ggc ttc tcc acc ccg ttc aac ttc ctc Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr Pro Phe Asn Phe Leu 600	605	610	3079
aac gcc cag tcc acc ttc acc ctt ggt gcg cag tcc ttc tcc aac cag Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln Ser Phe Ser Asn Gln 615	620	625	3127
gag gtc tac atc gac cgc gtc gag ttc gtc cca gcc gag gtc acc ttc Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro Ala Glu Val Thr Phe 630	635	640	3175
gag gcc gag tac gac ctg gag cgt gcc cag aag gcg gtg aac gcc ctg Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu 650	655	660	3223
ttc acc tcc acc aac ccc agg cgc ctg aag acc gac gtc acg gac tac Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr Asp Val Thr Asp Tyr 665	670	675	3271
cac atc gac cag gtg tcc aac atg gtg gcc tgc ctc tcc gac gag ttc His Ile Asp Gln Val Ser Asn Met Val Ala Cys Leu Ser Asp Glu Phe 680	685	690	3319
tgc ctg gac gag aag cgc gag ctg ttc gag aag gtc aag tac gcg aag Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys Val Lys Tyr Ala Lys 695	700	705	3367
cgc ctc tcc gac gag cgc aac ctg ctc cag gac ccg aac ttc acc ttc Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Thr Phe 710	715	720	3415
atc tcc ggc cag ctg tcc ttc gcg tcc atc gac ggc cag tcc aac ttc Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp Gly Gln Ser Asn Phe 730	735	740	3463
ccc tcc atc aac gag ctg tcc gag cac ggc tgg tgg ggc tcc gcg aac Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp Trp Gly Ser Ala Asn 745	750	755	3511
gtc acc atc cag gag ggc aac gac gtc ttc aag gag aac tac gtc acc Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys Glu Asn Tyr Val Thr 760	765	770	3559
ctg ccg ggc acc ttc aac gag tgc tac ccg aac tac ctc tac cag aag Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn Tyr Leu Tyr Gln Lys 775	780	785	3607
atc ggc gag tcc gag ctg aag gcc tac acc cgc tac cag ctg cgc gcc Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly 790	795	800	3655

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Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn	
810 815 820	
gcg aag cac gag acc ctg gac gtc cct ggc acg gac tcc ctg tgg ccc	3751
Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr Asp Ser Leu Trp Pro	
825 830 835	
ctc tcc gtc gag tgc ccc atc ggc cgc tgc ggc gag ccc aac cgc tgc	3799
Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys	
840 845 850	
gct ccc cac ttc gag tgg aac ccc gac ctg gac tgc tcc tgc cgc gac	3847
Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp	
855 860 865	
ggc gag cgc tgc gcg cac cat tcc cat cac ttc acc ctg gac atc gac	3895
Gly Glu Arg Cys Ala His His Ser His His Phe Thr Leu Asp Ile Asp	
870 875 880 885	
gtc ggc tgc acc gac ctg cac gag aac ctg ggc gtg tgg gtg gtc ttc	3943
Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly Val Trp Val Val Phe	
890 895 900	
aag atc aag acg cag gag ggc tac gcc cgc ctg ggc aac ctg gag ttc	3991
Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu Gly Asn Leu Glu Phe	
905 910 915	
atc gag gag aag cgc ctg atc ggc gag gcg ctc tcc cgc gtc aag cgt	4039
Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu Ser Arg Val Lys Arg	
920 925 930	
gcg gag aag aag tgg cgc gac aag cgc gag aag ctc cag ctg gag acc	4087
Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr	
935 940 945	
aag cgc gtc tac acc gag gcc aag gag gcc gtg gac gcc ctg ttc gtc	4135
Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val Asp Ala Leu Phe Val	
950 955 960 965	
gac tcc cag tac gac cag ctc cag gcg gac acc aac atc ggc atg atc	4183
Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Gly Met Ile	
970 975 980	
cat gcg gct gac aag ctg gtc cac cgc atc cgc gag gcg tac ctg tcc	4231
His Ala Ala Asp Lys Leu Val His Arg Ile Arg Glu Ala Tyr Leu Ser	
985 990 995	
gag ctg ccc gtc atc cct ggc gtc aac gcg gag atc ttc gag gag	4276
Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu Ile Phe Glu Glu	
1000 1005 1010	
ctg gag ggc cac atc atc acc gcc atg tcc ctc tac gac gcg cgc	4321
Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu Tyr Asp Ala Arg	
1015 1020 1025	
aac gtg gtc aag aac ggc gac ttc aac aac ggc ctg acg tgc tgg	4366
Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly Leu Thr Cys Trp	
1030 1035 1040	
aac gtc aag ggc cac gtc gac gtc cag caa tcc cac cac cgc tcc	4411
Asn Val Lys Gly His Val Asp Val Gln Gln Ser His His Arg Ser	
1045 1050 1055	
gac ctg gtc atc ccc gag tgg gag gcc gag gtg tcc cag gcc gtc	4456
Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Ala Val	
1060 1065 1070	
cgc gtc tgt ccg ggc agg ggc tac atc ctg cgc gtc acc gcg tac	4501
Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr	
1075 1080 1085	
aag gag ggc tac ggc gag ggc tgc gtc acg atc cac gag atc gag	4546
Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu	
1090 1095 1100	
aac aac acc gac gag ctg aag ttc aag aac tgc gag gag gag gag	4591
Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys Glu Glu Glu Glu	

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1105	1110	1115	
gtc tac ccg acg gac acc ggc acg tgc aac gac tac acc gcg cac Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala His 1120 1125 1130			4636
cag ggc acc gct gcc tgc aac tcc cgc aac gct ggc tac gag gac Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala Gly Tyr Glu Asp 1135 1140 1145			4681
gcc tac gag gtc gac acc acc gcc tcc gtc aac tac aag ccg acc Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr Lys Pro Thr 1150 1155 1160			4726
tac gag gag gag acc tac acc gac gtc cgt cgc gac aac cac tgc Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn His Cys 1165 1170 1175			4771
gag tac gac cgc ggc tac gtg aac tac cca ccc gtc ccc gct ggc Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala Gly 1180 1185 1190			4816
tac gtc acg aag gag ctg gag tac ttc ccc gag acc gac acc gtc Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val 1195 1200 1205			4861
tgg atc gag atc ggc gag acg gag ggc aag ttc atc gtc gac tcc Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser 1210 1215 1220			4906
gtc gag ctg ctc ctg atg gag gag tgatagaatt ctgcatgcgt Val Glu Leu Leu Leu Met Glu Glu 1225 1230			4950
ttggacgtat gctcattcag gttggagcca atttggttga tgtgtgtgcg agttcttgcg			5010
agtcctgatga gacatctctg tattgtgttt ctttccccag tgttttctgt acttggtgtaa			5070
tcggctaatac gccaacagat tcggcgatga ataaatgaga aataaattgt tctgattttg			5130
agtgcaaaaa aaaaggaatt agatctgtgt gtgttttttg			5170

<210> 12

<211> 1230

<212> PRT

<213> Artificial Sequence

<220>

<223> fully synthetic expression cassette

<400> 12

Met	Ala	Thr	Ser	Asn	Arg	Lys	Asn	Glu	Asn	Glu	Ile	Ile	Asn	Ala	Leu
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Ser	Ile	Pro	Thr	Val	Ser	Asn	Pro	Ser	Thr	Gln	Met	Asn	Leu	Ser	Pro
		20						25					30		

Asp	Ala	Arg	Ile	Glu	Asp	Ser	Leu	Cys	Val	Ala	Glu	Val	Asn	Asn	Ile
	35						40					45			

Asp	Pro	Phe	Val	Ser	Ala	Ser	Thr	Val	Gln	Thr	Gly	Ile	Asn	Ile	Ala
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Gly	Arg	Ile	Leu	Gly	Val	Leu	Gly	Val	Pro	Phe	Ala	Gly	Gln	Leu	Ala
65					70					75				80	

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Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp
85 90 95

Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln
100 105 110

Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu
115 120 125

Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp
130 135 140

Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val
145 150 155 160

Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg
165 170 175

Asn Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu
180 185 190

His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly
195 200 205

Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr
210 215 220

Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu
225 230 235 240

Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln
245 250 255

Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe
260 265 270

Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu
275 280 285

Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser
290 295 300

Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser
305 310 315 320

Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro
325 330 335

Glu Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln
340 345 350

His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly
355 360 365

Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile
370 375 380

Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu

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385          390          395          400
Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val
      405          410          415
Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg
      420          425          430
Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu
      435          440          445
Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn
      450          455          460
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly
      465          470          475          480
Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp
      485          490          495
Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val
      500          505          510
Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly
      515          520          525
Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
      530          535          540
Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val
      545          550          555          560
Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile
      565          570          575
Asn Gly Thr Thr Val Asn Ile Gly Asn Phe Ser Arg Thr Met Asn Arg
      580          585          590
Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr
      595          600          605
Pro Phe Asn Phe Leu Asn Ala Gln Ser Thr Phe Thr Leu Gly Ala Gln
      610          615          620
Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro
      625          630          635          640
Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys
      645          650          655
Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr
      660          665          670
Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys
      675          680          685
Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys
      690          695          700

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Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
705 710 715 720

Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp
725 730 735

Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp
740 745 750

Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys
755 760 765

Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn
770 775 780

Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg
785 790 795 800

Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr
805 810 815

Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr
820 825 830

Asp Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly
835 840 845

Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp
850 855 860

Cys Ser Cys Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe
865 870 875 880

Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly
885 890 895

Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu
900 905 910

Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu
915 920 925

Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys
930 935 940

Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val
945 950 955 960

Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr
965 970 975

Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg
980 985 990

Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu
995 1000 1005

Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu

1010

1015

1020

Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly
 1025 1030 1035

Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser
 1040 1045 1050

His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val
 1055 1060 1065

Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1070 1075 1080

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
 1085 1090 1095

His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys
 1100 1105 1110

Glu Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp
 1115 1120 1125

Tyr Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala
 1130 1135 1140

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn
 1145 1150 1155

Tyr Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg
 1160 1165 1170

Asp Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro
 1175 1180 1185

Val Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu
 1190 1195 1200

Thr Asp Thr Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe
 1205 1210 1215

Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1220 1225 1230

<210> 13

<211> 5600

<212> DNA

<213> Artificial Sequence

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<223> fully synthetic expression cassette

<220>

<221> promoter

<222> (26)..(640)

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<223> P-e35S

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<221> 5'UTL

<222> (665)..(735)

<223> L-Ta.CAB

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<221> Intron

<222> (749)..(1239)

<223> I-Os.ACT1

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<221> Transit_peptide

<222> (1255)..(1401)

<223> TP-Zm.rbcs

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<222> (1402)..(1564)

<223> I-Zm.rbcs

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<221> transit_peptide

<222> (1565)..(1651)

<223> TP-Zm.rbcs

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<221> CDS

<222> (1652)..(5341)

<223> Cry1Bb variant

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<221> transcription termination sequence

<222> (5342)..(5347)

<223> miscellaneous

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<221> polyadenylation sequence

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<222> (5350)..(5592)

<223> T-Os.LDH

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ccggaaacct cctcggattc cattgccagc ctatctgtca ctttattgtg aagatagtgg      120
aaaaggaagg tggctcctac aaatgccatc attgcgataa aggaaaggcc atcgttgaag      180
atgcctctgc cgacagtggc cccaagatg gacccccacc cacgaggagc atcgtggaaa      240
aagaagacgt tccaaccacg tcttcaaagc aagtggattg atgtgatggc ccgatgtgag      300
acttttcaac aaagggtaat atccggaaac ctccctcgat tccattgccc agctatctgt      360
cactttattg tgaagatagt ggaaaaggaa ggtggctcct acaaatgcc a tcattgcgat      420
aaaggaaagg ccacgcgttg agatgcctct gccgacagtg gtcccaaaga tggaccccc a      480
cccacgagga gcacgcgtga aaaagaagac gttccaacca cgtcttcaaa gcaagtggat      540
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gacaacacac cataagatcc aaggggaggc tccgccgccg ccggtaacca ccccgcccct      780
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tggtgtggcg agaggcggtc tcgtgcgcgc ccagatcggt gcgcgggagg ggcgggatct      900
cgcggtctgg gctctcgccg gcgtggatcc ggcccgatc tcgcggggaa tggggctctc      960
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cgtgctaaac aagatcagga agaggggaaa agggcactat ggtttatatt tttatatatt     1080
tctgctgctt cgtcaggcct agatgtgcta gatctttctt tcttcttttt gtgggtagaa     1140
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gcctcgtgcg gagctttttt gtaggtagaa gtgatcaacc tctagaggat cagcatggcg     1260
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gcagctgcag ctagcgagtt agtaatagga agggaaactg tgatccatgc atggactgat     1500
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gcaggtgtgg ccctacggca acaagaagtt cgagacgctg tcgtacctgc cgccgctgtc     1620
gaccggcggg cgcacccgct gcacgcaggc c atg gcc acc tcc aac cgc aag      1672
                               Met Ala Thr Ser Asn Arg Lys
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aac gag aat gag atc atc aac gcc ctg tcg atc ccc acg gtc tcg aac      1720
Asn Glu Asn Glu Ile Ile Asn Ala Leu Ser Ile Pro Thr Val Ser Asn
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ccg tcc acc caa atg aac ctg tcc ccg gac gcc cgc atc gag gac tcc      1768
Pro Ser Thr Gln Met Asn Leu Ser Pro Asp Ala Arg Ile Glu Asp Ser
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ctg tgc gtc gcg gag gtc aac aac atc gac ccc ttc gtc tcc gcc tcc      1816
Leu Cys Val Ala Glu Val Asn Asn Ile Asp Pro Phe Val Ser Ala Ser
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Gly Val Pro Phe Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe Leu Val	
75 80 85	
ggg gag ctg tgg ccc tcc ggt cgc gac ccc tgg gag atc ttc ctg gag	1960
Gly Glu Leu Trp Pro Ser Gly Arg Asp Pro Trp Glu Ile Phe Leu Glu	
90 95 100	
cac gtc gag cag ctc atc cgc cag caa gtc acc gag aac acc cgc aac	2008
His Val Glu Gln Leu Ile Arg Gln Gln Val Thr Glu Asn Thr Arg Asn	
105 110 115	
acg gcc atc gcc cgc ctg gag ggc ctg ggc cgt ggc tac cgc tcc tac	2056
Thr Ala Ile Ala Arg Leu Glu Gly Leu Gly Arg Gly Tyr Arg Ser Tyr	
120 125 130 135	
cag cag gcc ctg gag acc tgg ctg gac aac cgc aac gac gca cgc tcc	2104
Gln Gln Ala Leu Glu Thr Trp Leu Asp Asn Arg Asn Asp Ala Arg Ser	
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cgc tcc atc atc ctg gag cgc tac gtg gcg ctg gag ctg gac atc acc	2152
Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu Glu Leu Asp Ile Thr	
155 160 165	
acc gcc atc ccg ctc ttc cgc atc cgc aat gaa gag gtg ccc ctg ctc	2200
Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu Glu Val Pro Leu Leu	
170 175 180	
atg gtc tac gcc cag gct gcc aac ctg cac ctg ctc ctg ctt cgc gat	2248
Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp	
185 190 195	
gca tcc ctg ttc ggc tcc gag tgg ggc atg gcc tcg tcc gac gtc aac	2296
Ala Ser Leu Phe Gly Ser Glu Trp Gly Met Ala Ser Ser Asp Val Asn	
200 205 210 215	
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Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr Thr Glu Glu Tyr Ser Asn His	
220 225 230	
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Cys Val Gln Trp Tyr Asn Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn	
235 240 245	
gct gag tcc tgg ctg cgc tac aac cag ttc cgc cgc gac ctg acg ctg	2440
Ala Glu Ser Trp Leu Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu	
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Gly Val Leu Asp Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr	
265 270 275	
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Tyr Pro Ile Asn Thr Ser Ala Gln Leu Thr Arg Glu Ile Tyr Thr Asp	
280 285 290 295	
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Pro Ile Gly Arg Thr Asn Ala Pro Ser Gly Phe Ala Ser Thr Asn Trp	
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Phe Asn Asn Asn Ala Pro Ser Phe Ser Ala Ile Glu Ala Ala Ile Phe	
315 320 325	
cgc cca ccg cac ctc ctg gac ttc ccc gag cag ctg acc atc tac tcc	2680
Arg Pro Pro His Leu Leu Asp Phe Pro Glu Gln Leu Thr Ile Tyr Ser	
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gcc tcg tcc cgc tgg tcg tcc acc cag cac atg aac tac tgg gtg ggc	2728
Ala Ser Ser Arg Trp Ser Ser Thr Gln His Met Asn Tyr Trp Val Gly	
345 350 355	
cac cgc ctc aac ttc agg ccc atc ggt ggc acc ctg aac acc tcc acc	2776
His Arg Leu Asn Phe Arg Pro Ile Gly Gly Thr Leu Asn Thr Ser Thr	

360	365	370	375	
cag ggc ctg acc aac aac acc tcc atc aac ccc gtc acc ctc cag ttc				2824
Gln Gly Leu Thr Asn Asn Thr Ser Ile Asn Pro Val Thr Leu Gln Phe	380	385	390	
acg tcc cgc gac gtc tac cgc acc gag tcc aac gcc ggc acc aac atc				2872
Thr Ser Arg Thr 395 Val Tyr Arg Thr Gly Val 400 Ser Asn Ala Gly Thr Asn Ile		405		
ctc ttc acg acc ccg gtc aac ggc gtc ccc tgg gct cgc ttc aac ttc				2920
Leu Phe Thr Thr Pro Val Asn Gly Val Pro Trp Ala Arg Phe Asn Phe	410	415	420	
atc aac ccg cag aac atc tac gag cgt ggt gcg acc acc tac tcc cag				2968
Ile Asn Pro Gln Asn Ile Tyr 430 Glu Arg Gly Ala Thr Thr Tyr Ser Gln	425	435		
ccg tac cag ggc gtc ggc atc cag ctc ttc gac tcc gag acc gag ctg				3016
Pro Tyr Gln Gly Val Gly Ile Gln Leu Phe Asp Ser Glu Thr Glu Leu	440	445	455	
cca ccc gag acg acc gag cgt ccc aac tac gag tcc tac tcc cac cgc				3064
Pro Pro Glu Thr 460 Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg	465	470		
ctg tcc cac atc ggc ctg atc atc ggc aac acc ctc agg gct ccc gtc				3112
Leu Ser His Ile Gly Leu Ile Ile Gly Asn Thr Leu Arg Ala Pro Val	475	480	485	
tac tcc tgg acg cac cgc tcc gcg gac cgc acg aac acg atc ggt ccc				3160
Tyr Ser Trp Thr His Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro	490	495	500	
aac cgc atc acc cag atc ccc ctg gtc aag gcc ctc aac ctg cac tcc				3208
Asn Arg Ile Thr Gln Ile Pro Leu Val Lys Ala Leu Asn Leu His Ser	505	510	515	
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Gly Val Thr Val Val Gly Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	520	525	535	
cgc agg acc aac acg ggc acc ttc ggc gac atc cgc ctc aac atc aac				3304
Arg Arg Thr Asn Thr Gly Thr Phe Gly Asp Ile Arg Leu Asn Ile Asn	540	545	550	
gtc ccg ctg tcc cag cgc tac cgc gtc cgc atc cgc tac gcc tcc acg				3352
Val Pro Leu Ser 555 Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr	560	565		
acc gac ctc cag ttc ttc acg cgc atc aac ggc acc acg gtc aac atc				3400
Thr Asp Leu Gln Phe Phe Thr Arg Ile Asn Gly Thr Thr Val Asn Ile	570	575	580	
ggc aac ttc tcc cgc acc atg aac agg ggc gac aac ctg gag tac cgc				3448
Gly Asn Phe Ser Arg Thr Met 590 Asn Arg Gly Asp Asn Leu Glu Tyr Arg	585	595		
tcc ttc cgc acc gcc ggc ttc tcc acc ccg ttc aac ttc ctc aac gcc				3496
Ser Phe Arg Thr Ala Gly Phe Ser Thr Pro Phe Asn Phe Leu Asn Ala	600	605	615	
cag tcc acc ttc acc ctt ggt gcg cag tcc ttc tcc aac cag gag gtc				3544
Gln Ser Thr Phe Thr Leu Gly Ala Gln Ser Phe Ser Asn Gln Glu Val	620	625	630	
tac atc gac cgc gtc gag ttc gtc cca gcc gag gtc acc ttc gag gcc				3592
Tyr Ile Asp Arg Val Glu Phe Val Ala Glu Val Thr Phe Glu Ala	635	640	645	
gag tac gac ctg gag cgt gcc cag aag gcg gtg aac gcc ctg ttc acc				3640
Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr	650	655	660	
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Ser Thr Asn Pro Arg Arg Leu Lys Thr Asp Val Thr Asp Tyr His Ile	665	670	675	

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gac	gag	aag	cgc	gag	ctg	ttc	gag	aag	gtc	aag	tac	gcg	aag	cgc	ctc		3784
Asp	Glu	Lys	Arg	Glu	Leu	Phe	Glu	Lys	Val	Lys	Tyr	Ala	Lys	Arg	Leu		
				700					705					710			
tcc	gac	gag	cgc	aac	ctg	ctc	cag	gac	ccg	aac	ttc	acc	ttc	atc	tcc		3832
Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	Phe	Thr	Phe	Ile	Ser		
				715				720					725				
ggc	cag	ctg	tcc	ttc	gcg	tcc	atc	gac	ggc	cag	tcc	aac	ttc	ccc	tcc		3880
Gly	Gln	Leu	Ser	Phe	Ala	Ser	Ile	Asp	Gly	Gln	Ser	Ala	Asn	Phe	Pro	Ser	
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atc	aac	gag	ctg	tcc	gag	cac	ggc	tgg	tgg	ggc	tcc	gcg	aac	gtc	acc		3928
Ile	Asn	Glu	Leu	Ser	Glu	His	Gly	Trp	Trp	Gly	Ser	Ala	Asn	Val	Thr		
				745				750				755					
atc	cag	gag	ggc	aac	gac	gtc	ttc	aag	gag	aac	tac	gtc	acc	ctg	ccg		3976
Ile	Gln	Glu	Gly	Asn	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	Thr	Leu	Pro		
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ggc	acc	ttc	aac	gag	tgc	tac	ccg	aac	tac	ctc	tac	cag	aag	atc	ggc		4024
Gly	Thr	Phe	Asn	Glu	Cys	Tyr	Pro	Asn	Tyr	Leu	Tyr	Gln	Lys	Ile	Gly		
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Glu	Ser	Glu	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	Gly	Tyr	Ile		
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cac	gag	acc	ctg	gac	gtc	cct	ggc	acg	gac	tcc	ctg	tgg	ccc	ctc	tcc		4168
His	Glu	Thr	Leu	Asp	Val	Pro	Gly	Thr	Asp	Ser	Leu	Trp	Pro	Leu	Ser		
				825					830				835				
gtc	gag	tgc	ccc	atc	ggc	cgc	tgc	ggc	gag	ccc	aac	cgc	tgc	gct	ccc		4216
Val	Glu	Ser	Pro	Ile	Gly	Arg	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro		
				845					850						855		
cac	ttc	gag	tgg	aac	ccc	gac	ctg	gac	tgc	tcc	tgc	cgc	gac	ggc	gag		4264
His	Phe	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu		
				860					865					870			
cgc	tgc	gcg	cac	cat	tcc	cat	cac	ttc	acc	ctg	gac	atc	gac	gtc	ggc		4312
Arg	Cys	Ala	His	His	Ser	His	His	Phe	Thr	Leu	Asp	Ile	Asp	Val	Gly		
				875					880				885				
tgc	acc	gac	ctg	cac	gag	aac	ctg	ggc	gtg	tgg	gtg	gtc	ttc	aag	atc		4360
Cys	Thr	Asp	Leu	His	Glu	Asn	Leu	Gly	Val	Trp	Val	Val	Phe	Lys	Ile		
				890				895					900				
aag	acg	cag	gag	ggc	tac	gcc	cgc	ctg	ggc	aac	ctg	gag	ttc	atc	gag		4408
Lys	Thr	Gln	Glu	Gly	Tyr	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Ile	Glu		
				905				910				915					
gag	aag	ccg	ctg	atc	ggc	gag	gcg	ctc	tcc	cgc	gtc	aag	cgt	gcg	gag		4456
Glu	Lys	Pro	Leu	Ile	Gly	Glu	Ala	Leu	Ser	Arg	Val	Lys	Arg	Ala	Glu		
				925					930						935		
aag	aag	tgg	cgc	gac	aag	cgc	gag	aag	ctc	cag	ctg	gag	acc	aag	cgc		4504
Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Lys	Arg		
				940					945					950			
gtc	tac	acc	gag	gcc	aag	gag	gcc	gtg	gac	gcc	ctg	ttc	gtc	gac	tcc		4552
Val	Tyr	Thr	Glu	Ala	Lys	Glu	Ala	Val	Asp	Ala	Leu	Phe	Val	Asp	Ser		
				955				960					965				
cag	tac	gac	cag	ctc	cag	gcg	gac	acc	aac	atc	ggc	atg	atc	cat	gcg		4600
Gln	Tyr	Asp	Gln	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Gly	Met	Ile	His	Ala		
				970				975					980				
gct	gac	aag	ctg	gtc	cac	cgc	atc	cgc	gag	gcg	tac	ctg	tcc	gag	ctg		4648
Ala	Asp	Lys	Leu	Val	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Ser	Glu	Leu		

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ggc tac ggc gag ggc tgc gtc acg atc cac gag atc gag aac aac Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn 1090 1095 1100			4963
acc gac gag ctg aag ttc aag aac tgc gag gag gag gag gtc tac Thr Asp Glu Leu Lys Phe Lys Asn Cys Glu Glu Glu Val Tyr 1105 1110 1115			5008
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<213> Artificial Sequence

<220>

<223> fully synthetic expression cassette

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Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr Gly Ile Asn Ile Ala
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Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe Ala Gly Gln Leu Ala
65 70 75 80

Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp Pro Ser Gly Arg Asp
85 90 95

Pro Trp Glu Ile Phe Leu Glu His Val Glu Gln Leu Ile Arg Gln Gln
100 105 110

Val Thr Glu Asn Thr Arg Asn Thr Ala Ile Ala Arg Leu Glu Gly Leu
115 120 125

Gly Arg Gly Tyr Arg Ser Tyr Gln Gln Ala Leu Glu Thr Trp Leu Asp
130 135 140

Asn Arg Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val
145 150 155 160

Ala Leu Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg
165 170 175

Asn Glu Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu
180 185 190

His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe Gly Ser Glu Trp Gly
195 200 205

Met Ala Ser Ser Asp Val Asn Gln Tyr Tyr Gln Glu Gln Ile Arg Tyr
210 215 220

Thr Glu Glu Tyr Ser Asn His Cys Val Gln Trp Tyr Asn Thr Gly Leu
225 230 235 240

Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Leu Arg Tyr Asn Gln
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Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp Leu Val Ala Leu Phe

260

265

270

Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn Thr Ser Ala Gln Leu
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 Thr Arg Glu Ile Tyr Thr Asp Pro Ile Gly Arg Thr Asn Ala Pro Ser
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 Gly Phe Ala Ser Thr Asn Trp Phe Asn Asn Asn Ala Pro Ser Phe Ser
 305 310 315 320
 Ala Ile Glu Ala Ala Ile Phe Arg Pro Pro His Leu Leu Asp Phe Pro
 325 330 335
 Glu Gln Leu Thr Ile Tyr Ser Ala Ser Ser Arg Trp Ser Ser Thr Gln
 340 345 350
 His Met Asn Tyr Trp Val Gly His Arg Leu Asn Phe Arg Pro Ile Gly
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 Gly Thr Leu Asn Thr Ser Thr Gln Gly Leu Thr Asn Asn Thr Ser Ile
 370 375 380
 Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg Thr Glu
 385 390 395 400
 Ser Asn Ala Gly Thr Asn Ile Leu Phe Thr Thr Pro Val Asn Gly Val
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 Pro Trp Ala Arg Phe Asn Phe Ile Asn Pro Gln Asn Ile Tyr Glu Arg
 420 425 430
 Gly Ala Thr Thr Tyr Ser Gln Pro Tyr Gln Gly Val Gly Ile Gln Leu
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 Phe Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr Glu Arg Pro Asn
 450 455 460
 Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ile Gly
 465 470 475 480
 Asn Thr Leu Arg Ala Pro Val Tyr Ser Trp Thr His Arg Ser Ala Asp
 485 490 495
 Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln Ile Pro Leu Val
 500 505 510
 Lys Ala Leu Asn Leu His Ser Gly Val Thr Val Val Gly Gly Pro Gly
 515 520 525
 Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
 530 535 540
 Asp Ile Arg Leu Asn Ile Asn Val Pro Leu Ser Gln Arg Tyr Arg Val
 545 550 555 560
 Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe Phe Thr Arg Ile
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 Gly Asp Asn Leu Glu Tyr Arg Ser Phe Arg Thr Ala Gly Phe Ser Thr
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 610 615 620

 Ser Phe Ser Asn Gln Glu Val Tyr Ile Asp Arg Val Glu Phe Val Pro
 625 630 635 640

 Ala Glu Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys
 645 650 655

 Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Pro Arg Arg Leu Lys Thr
 660 665 670

 Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Met Val Ala Cys
 675 680 685

 Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Phe Glu Lys
 690 695 700

 Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
 705 710 715 720

 Pro Asn Phe Thr Phe Ile Ser Gly Gln Leu Ser Phe Ala Ser Ile Asp
 725 730 735

 Gly Gln Ser Asn Phe Pro Ser Ile Asn Glu Leu Ser Glu His Gly Trp
 740 745 750

 Trp Gly Ser Ala Asn Val Thr Ile Gln Glu Gly Asn Asp Val Phe Lys
 755 760 765

 Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn Glu Cys Tyr Pro Asn
 770 775 780

 Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu Lys Ala Tyr Thr Arg
 785 790 795 800

 Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr
 805 810 815

 Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu Asp Val Pro Gly Thr
 820 825 830

 Asp Ser Leu Trp Pro Leu Ser Val Glu Ser Pro Ile Gly Arg Cys Gly
 835 840 845

 Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp Asn Pro Asp Leu Asp
 850 855 860

 Cys Ser Cys Arg Asp Gly Glu Arg Cys Ala His His Ser His His Phe
 865 870 875 880

 Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu His Glu Asn Leu Gly

885

890

895

Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu Gly Tyr Ala Arg Leu
900 905 910

Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu Ile Gly Glu Ala Leu
915 920 925

Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys
930 935 940

Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu Ala Lys Glu Ala Val
945 950 955 960

Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr
965 970 975

Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu Val His Arg Ile Arg
980 985 990

Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro Gly Val Asn Ala Glu
995 1000 1005

Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr Ala Met Ser Leu
1010 1015 1020

Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe Asn Asn Gly
1025 1030 1035

Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln Gln Ser
1040 1045 1050

His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu Val
1055 1060 1065

Ser Gln Ala Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1070 1075 1080

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile
1085 1090 1095

His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Cys
1100 1105 1110

Glu Glu Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp
1115 1120 1125

Tyr Thr Ala His Gln Gly Thr Ala Ala Cys Asn Ser Arg Asn Ala
1130 1135 1140

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn
1145 1150 1155

Tyr Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg
1160 1165 1170

Asp Asn His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro
1175 1180 1185

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Val	Pro	Ala	Gly	Tyr	Val	Thr	Lys	Glu	Leu	Glu	Tyr	Phe	Pro	Glu
1190						1195					1200			

Thr	Asp	Thr	Val	Trp	Ile	Glu	Ile	Gly	Glu	Thr	Glu	Gly	Lys	Phe
1205						1210					1215			

Ile	Val	Asp	Ser	Val	Glu	Leu	Leu	Leu	Met	Glu	Glu
1220						1225					1230